AMENDMENTS TO THE CLAIMS

- 1. (currently amended) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:
 - a) collecting a tissue sample from a human subject;
- b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and
- c) detecting in the amplification products the presence or absence of a twelvefold CA dinucleotide repeat consisting of (SEQ. ID. NO.:6), wherein said CA
 dinucleotide repeat sequence is located in the genomic sequence upstream from a

 PARP transcription start site, corresponding to nucleotide positions 846 through 869 of
 (SEQ. ID. NO.:5), and wherein the presence of said twelve-fold CA dinucleotide repeat
 sequence is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic
 predisposition to develop SLE in a subject not presenting SLE symptoms.
- 2. (currently amended) The method of Claim 1, further comprising:

 detecting in the amplification products the presence or absence of an eighteenfold CA dinucleotide repeat consisting of (SEQ. ID. NO.:7), wherein said eighteen-fold

 CA dinucleotide repeat sequence is located in the genomic sequence upstream from a

 PARP transcription start site, between nucleotide positions 845 and 869 of (SEQ. ID.

 NO.:5), and wherein the absence of said eighteen-fold CA dinucleotide repeat

 sequence is diagnostic of SLE in subject having SLE symptoms or indicates a genetic

 predisposition to develop SLE in a subject not presenting SLE symptoms.

- 3. (original) The method of Claim 1, wherein the tissue sample is a blood sample.
- 4. (original) The method of Claim 1, wherein an oligonucleotide primer is used in amplifying said nucleic acids.
- 5. (original) The method of Claim 4, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.
- 6. (original) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.
- 7. (original) The method of Claim 4, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.
- 8. (original) The method of Claim 4, wherein said oligonucleotide primer is labeled with a fluorescent dye.
- 9. (original) The method of Claim 8, wherein said dye is SYBR Green I, YO-PRO-1, thiazole orange, Hex, FAM or TET.

10-11. (canceled)

12. (currently amended) A genetic testing method for systemic lupus erythematosus (SLE) in a human subject, comprising:

- a) collecting a tissue sample from a human subject;
- b) amplifying nucleic acids from said tissue sample to obtain amplification products, said nucleic acids comprising a genomic sequence of human chromosome 1 between microsatellite markers D1S2860 and D1S213; and
- c) detecting in the amplification products the presence or absence of an eighteen-fold CA dinucleotide repeat sequence consisting of (SEQ. ID. NO.:7), wherein said eighteen-fold CA dinucleotide repeat sequence is located in the genomic sequence upstream from a *PARP* transcription start site, between nucleotide positions 845 and 869 of (SEQ. ID. NO.:5), and wherein the absence of said eighteen-fold CA dinucleotide repeat sequence is diagnostic of SLE in a subject having SLE symptoms or indicates a genetic predisposition to develop SLE in a subject not presenting SLE symptoms.
- 13. (original) The method of Claim 12, wherein the tissue sample is a blood sample.
- 14. (original) The method of Claim 12, wherein an oligonucleotide primer is used in amplifying said nucleic acids.
- 15. (original) The method of Claim 14, wherein said primer has a nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID. NO.:1) or a fragment thereof at least 18 nucleotides long, or AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long.
- 16. (original) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence GAT TCC CCA TCT CTC TTT CTT T (SEQ. ID.

- NO.:1) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.
- 17. (original) The method of Claim 14, wherein an oligonucleotide primer comprising nucleotide sequence AAA TTG TGG TAA TGA CTG CA (SEQ. ID. NO.:2) or a fragment thereof at least 18 nucleotides long, is used in amplifying said nucleic acids.
- 18. (original) The method of Claim 14, wherein said oligonucleotide primer is labeled with a fluorescent dye.
- 19. (original) The method of Claim 18, wherein said dye is SYBR Green I, YO-PRO-1, thiazole orange, Hex, FAM or TET.